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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/899,295

DATE: 07/24/2001
TIME: 10:54:05

Input Set : A:\00a033e1.app
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3 <110> APPLICANT: Aventis Pharma Deutschland GmbH
 5 <120> TITLE OF INVENTION: Process for identifying modulators of G protein coupled
 6 receptors
 8 <130> FILE REFERENCE: AVE D-2000/A033 englisch
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/899,295
 C--> 11 <141> CURRENT FILING DATE: 2001-07-06
 13 <160> NUMBER OF SEQ ID NOS: 10
 15 <170> SOFTWARE: PatentIn Ver. 2.1
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 18 <211> LENGTH: 1080
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
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 25 aagctgctgc tgctcggac aggagagagt ggcaagagta cgtttatcaa gcagatgaga 180
 26 atcatccatg ggtcaggata ctctgatgaa gataaaaggg gttcaccaa gctggtgtat 240
 27 cagaacatct tcacggccat gcaggccatg atcagagcca tggacacact caagatccca 300
 28 tacaagtatg agcacaataa ggctcatgca caatttagttc gagaagttga tgtggagaag 360
 29 gtgtctgctt ttgagaatcc atatgttagat gcaataaaga gtttatggaa tgatctgg 420
 30 atccaggaat gctatgatag acgacgagaa tatcaattat ctgactctac caaatactat 480
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 32 agagttcgag tccccaccac agggatcatc gaataccct ttgacttaca aagtgtcatt 600
 33 ttcagaatgg tcgatgttagg gggccaaagg tcagagagaa gaaaatggat acactgctt 660
 34 gaaaatgtca cctctatcat gttctagta gcgccttagt aatatgatca agtttcgtg 720
 35 gagtcagaca atgagaacct aatggaggaa agcaaggctc tctttagaac aattatcaca 780
 36 tacccttgtt tccagaactc ctcggttatt ctgttcttaa acaagaaaga tcttcttagag 840
 37 gagaaaatca tgtattccca tctagtcgac tacttccag aatatgatgg accccagaga 900
 38 gatgcccgagg cagcccgaga attcattctg aagatgttg tggacctgaa cccagacagt 960
 39 gacaaaatta tctactccca cttcacgtgc gccacagaca ccgagaatat ccgcttgtc 1020
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 45 <212> TYPE: PRT
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 53 20 25 30
 55 Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Gly Thr Gly
 56 35 40 45
 58 Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
 59 50 55 60
 61 Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
 62 65 70 75 80
 64 Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr

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71	115	120	125
73	Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys		
74	130	135	140
76	Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr		
77	145	150	155
79	160		
80	Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln		
82	165	170	175
83	Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr		
85	180	185	190
86	Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val Asp Val Gly Gly		
88	195	200	205
89	Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr		
91	210	215	220
92	Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val		
94	225	230	235
95	240		
97	Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg		
98	245	250	255
99	Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe		
100	260	265	270
101	Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu		
103	275	280	285
104	Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala		
106	290	295	300
107	Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser		
109	305	310	315
110	320		
112	Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn		
113	325	330	335
115	Ile Arg Phe Val Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn		
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128	acaggagaga gtggcaagag tacgtttatac aagcagatga gaatcatcca tgggtcagga 180		
129	tactctgatg aagataaaaag gggcttcacc aagctggtgt atcagaacat cttcacggcc 240		
130	atgcaggcca tgatcagagc catggacaca ctcaagatcc catacaagta tgagcacaat 300		
131	aaggctcatg cacaattagt tcgagaagg t gatgtggaga aggtgtctgc ttttggaaat 360		
132	ccatatgttag atgcaataaa gagtttatgg aatgatcctg gaatccagga atgctatgat 420		
133	agacgacgag aatatacaatt atctgactt accaaatact atcttaatga cttggaccgc 480		
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 136 gggggccaaa ggtcagagag aagaaaaatgg atacactgct ttgaaaatgt caccctatc 660
 137 atgttcttag tagcgtttag tgaatatgtt caagttctcg tggagtcaga caatgagaac 720
 138 cgaatggagg aaagcaaggc tctctttaga acaattatca catacccttg gttccagaac 780
 139 tcctcggtta ttctgttctt aaacaagaaa gatcttctag aggagaaaaat catgtattcc 840
 140 catctagtcg actacttccc agaatatgtt ggacccaga gagatgccca ggcagccga 900
 141 gaattcatttc tgaagatgtt cgtggacctg aaccagaca gtgacaaaat tatctactcc 960
 142 cacttcacgt gcgcacaga caccgagaat atccgctttg tcttgctgc cgtcaaggac 1020
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 155 Asp Glu Ile Glu Arg His Val Arg Arg Asp Lys Arg Asp Ala Arg Arg
 156 20 25 30
 158 Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr
 159 35 40 45
 161 Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu
 162 50 55 60
 164 Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala
 165 65 70 75 80
 167 Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys
 168 85 90 95
 170 Tyr Glu His Asn Lys Ala His Ala Gln Leu Val Arg Glu Val Asp Val
 171 100 105 110
 173 Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser
 174 115 120 125
 176 Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu
 177 130 135 140
 179 Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg
 180 145 150 155 160
 182 Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val
 183 165 170 175
 185 Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser
 186 180 185 190
 188 Val Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg
 189 195 200 205
 191 Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile Met Phe Leu Val
 192 210 215 220
 194 Ala Leu Ser Glu Tyr Asp Gln Val Leu Val Glu Ser Asp Asn Glu Asn
 195 225 230 235 240
 197 Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro
 198 245 250 255
 200 Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu
 201 260 265 270
 203 Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp Tyr Phe Pro Glu

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204	275	280	285
206	Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu		
207	290	295	300
209	Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser		
210	305	310	315
212	His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala		320
213	325	330	335
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231	acaggagaga gtggcaagag tacgtttatc aagcagatga gaatcatcca tgggtcagga 180		
232	tactctgatg aagataaaag gggcttcacc aagctggtgt atcagaacat cttcacggcc 240		
233	atgcaggcca tgatcagac catggacaca ctcaagatcc catacaagta tgagcacaat 300		
234	aaggctcatg cacaattagt tcgagaagtt gatgtggaga aggtgtctgc ttttgagaat 360		
235	ccatatatgtat atgcaataaa gagtttatgg aatgatcctg gaatccagga atgtatgtat 420		
236	agacgacgag aatatcaatt atctgactt accaaatact atcttaatga cttggaccgc 480		
237	gtagctgacc ctgcctacct gcctacgcaa caagatgtgc tttagagttcg agtccccacc 540		
238	acagggatca tcgaataaccc ctttgactta caaagtgtca ttttcagaat ggtcgatgt 600		
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261	Glu Leu Lys Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr		
262	35 40 45		
264	Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu		
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270	Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys		

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273	Tyr Glu His Asn Lys Ala His Ala Gln Leu Val Arg Glu Val Asp Val		
274	100	105	110
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277	115	120	125
279	Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu		
280	130	135	140
282	Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg		
283	145	150	155
285	160	165	170
286	Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val		
288	180	185	190
289	Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser		
291	190	195	200
292	Val Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg		
294	205	210	215
295	Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile Met Phe Leu Val		
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298	235	240	240
300	Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro		
301	245	250	255
303	Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu		
304	260	265	270
306	Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp Tyr Phe Pro Glu		
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309	Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu		
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312	Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser		
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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date